## SEQUENCE LISTING

<110> Walker, Ameae M.

<120> PROLACTIN ANTAGONISTS AND USES THEREOF

<130> Walker\_2500\_097US2

<140> 09/065,330

<141> 1998-04-23

<150> PCT/US97/01435

<151> 1997-01-30

<150> 08/594,809

<151> 1996-01-31

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 832

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (622)..(624)

<223> This is the codon for the substituted amino acids of the mutated sequence.

aacatgaaca tcaaaggatc gccatggaaa gggtccctcc tgctgctgct ggtgtcaaac 60 ctgctgctgt gccagagcgt ggcccccttg cccatctgtc ccggcggggc tgcccgatgc 120 caggtgaccc ttcgagacct gtttgaccgc gccgtcgtcc tgtcccacta catccataac 180 ctctcctcag aaatgttcag cgaattcgat aaacggtata cccatggccg ggggttcatt 240 accaaggcca tcaacagctg ccacacttct tcccttgcca cccccgaaga caaggagcaa 300 gcccaacaga tgaatcaaaa agactttctg agcctgatag tcagcatatt gcgatcctgg 360 aatgagcctc tgtatcatct ggtcacggaa gtacgtggta tgcaagaagc cccggaggct 420 ctgatagtca gccaggttca tcctgaaacc aaagaaaatg agatctaccc tgtctggtcg 540 ggacttccat ccctgcagat ggctgatgaa gagtctcgcc tttctgctta ttataacctg 600 ctccactgcc tacgcaggga tnnncataaa atcgacaatt atctcaagct cctgaagtgc 660 cgaatcatcc acaacaacaa ctgctaagcc cacatccatt tcatctattt ctgagaaggt 720 ccttaatgat ccgttccatt gcaagcttct tttagttgta tftcttttga atccatgctt 780 gggtgtaaca ggtctcctct taaaaaataa aaactgactc gtagagaca tc

<210> 2

<211> 227

3 .

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (208)

<223> Site mutated codon where the normal codon coding for serine is modified preferably to encode for aspartate or glutamate, most preferably aspartate.

Asn Met Asn Ile Lys Gly Ser Pro Trp Lys Gly Ser Leu Leu Leu <400> 2 10 5 1

Leu Val Ser Asn Leu Leu Cys Gln Ser Val Ala Pro Leu Pro Ile 25 20

Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu Arg Asp Leu Phe 40 35

Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn Leu Ser Ser Glu 55 50

Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly Arg Gly Phe Ile 75 70 65

Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu Ala Thr Pro Glu 90 85

Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp Phe Leu Ser Leu 105 100

Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu Tyr His Leu Val 120 115

Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala Ile Leu Ser Lys 140 135 130

Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu Glu Gly Met Glu 155 150 145

Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu Asn Glu Ile Tyr 170 165

Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala Asp Glu Glu Ser

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2

190 185 180

Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu Arg Arg Asp Xaa 205 200 195

His Lys Ile Asp Asn Tyr Leu Lys Leu Leu Lys Cys Arg Ile Ile His 220 215 210

Asn Asn Asn Cys 225

<210> 3

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: This sequence is a primer.

<400> 3 gcagggatga ccacaaggtt gac

23

<210> 4

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: This sequence is a primer.

<220>

<221> variation

<222> (12)

<223> This is a codon that can be replaced for nucleic acid substitutes.

<400> 4

cgcaagggat gnacacaagg ttga

24

<210> 5

<211> 22

<212> DNA

3

<213> Artificial Sequence <223> Description of Artificial Sequence: This sequence is a primer. <220> <221> variation <222> (12) <223> This is a codon that can be replaced for nucleic acid substitutes. <400> 5 22 acgcagggat gnkataaaat cg <210> 6 <211> 26 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: This sequence <220> is a primer. <400> 6 26

cgtggccccc atatgttgcc catctg

4